WHAT IS CLAIMED IS:

1. An isolated virulent gene of *L. monocytogenes*.

2. The isolated gene of Claim 1, wherein said gene encodes a protein having virulent biological activity.

3. The isolated gene of Claim 1, wherein said gene comprises a nucleic acid molecule selected from the group consisting of SEQ ID NOS.: 1-9.

4. The isolated gene of Claim 3, wherein said gene encodes a protein having virulent biological activity.

5. The isolated gene of Claim 1, wherein said gene comprises a nucleic acid molecule having 95 % sequence homology to a nucleic acid molecule selected from the group consisting of SEQ ID NOS.: 1-9.

6. The isolated gene of Claim 1, wherein said gene comprises a nucleic acid molecule having 90 % sequence homology to a nucleic acid molecule selected from the group consisting of SEQ ID NOS.: 1-9.

7. The isolated gene of Claim 1, wherein said gene comprises a nucleic acid molecule having 80 % sequence homology to a nucleic acid molecule selected from the group consisting of SEQ ID NOS.: 1-9.

8. The isolated gene of Claim 1, wherein said gene comprises a nucleic acid molecule that binds to a specific primer or probe, said primer or probe being selected from the group consisting of SEQ ID NOS.: 10-27.

9. The isolated gene of Claim 1, wherein said gene comprises a nucleic acid molecule that binds to a polynucleotide fragment having 95 % sequence

homology to a primer or probe selected from the group consisting of SEQ ID NOS.: 10-27.

10. The isolated gene of Claim 1, wherein said gene comprises a nucleic acid molecule that binds to a polynucleotide fragment having 90 % sequence homology to a primer or probe selected from the group consisting of SEQ ID NOS.: 10-27.

11. The isolated gene of Claim 1, wherein said gene comprises a nucleic acid molecule that binds to a polynucleotide fragment having 80 % sequence homology to a primer or probe selected from the group consisting of SEQ ID NOS.: 10-27.

12. The isolated gene of Claim 1, wherein said gene comprises a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-9.

13. A novel primer or probe for the identification of virulent genes of *L. monocytogenes*, said primer or probe being a polynucleotide fragment of at least 10 base pairs that bind to or are complementary with a portion of at least one polynucleotide selected from the group consisting of SEQ ID NOS.: 1-9.

14. A novel primer or probe for the identification of virulent genes of L. monocytogenes, said primer or probe being selected from the group consisting of SEQ ID NOS.: 10-27.

15. A method of identifying virulent *a L. monocytogenes* isolate comprising:

providing at least one primer or probe specific for a corresponding at least one virulence-specific gene of *L. monocytogenes*;

conducting PCR assay or hybridization using said at least one primer or probe to identify the presence of said corresponding at least one virulence-specific gene in said *L. monocytogenes* isolate.

16. The method of Claim 15, wherein said virulence-specific gene is selected from the group consisting of genes identified by SEQ ID NOS.: 1-9.

17. The method of Claim 15, wherein said at least one primer is selected from the group consisting of SEQ ID NOS.: 10-27.

18. The method of Claim 15, wherein said at least one primer or probe is two or more primers or probes and said corresponding at least one virulence-specific gene is two or more virulence-specific genes and said PCR assay or hybridization is multiplex polymerase chain reaction or hybridization.

19. The method of Claim 15, wherein said PCR assay or hybridization is multiplex polymerase chain reaction or hybridization using said primers or probes specific for said virulence-specific gene in combination with *Listeria* genus-specific primers or probes or *L. moncytogenes* species-specific gene sequence.

20. The method of Claim 15, wherein said *L. monocytogenes* species-specific gene sequence is selected from the from the group consisting of genes identified by SEQ ID NOS.: 28-33.

21. The method of Claim 15, wherein said PCR assay or hybridization is multiplex polymerase chain reaction or hybridization using said primers or probes specific for said virulence-specific gene in combination with *Listeria* genus-specific primers or probes and *L. moncytogenes* species-specific gene sequence.

22. The method of Claim 17, wherein said *L. monocytogenes* species-specific gene sequence is selected from the from the group consisting of genes identified by SEQ ID NOS.: 28-33.

23. The method of Claim 15, wherein said at least one virulence-specific gene is involved in inhibition of growth.

24. The method of Claim 15, wherein said at least one virulence-specific gene is involved in reduction of pathogenicty.

25. The method of Claim 15, wherein said at least one virulence-specific gene is involved in treatment of pathogenicity.

26. The method of Claim 15, wherein said at least one virulence-specific gene is involved in the prevention of virulent strains of *L. monocytogenes*.

27. The method of Claim 15, wherein said at least one virulence-specific gene is detected by amplification of said genes from mRNA and said PCR is reverse transcriptase-PCR (RT-PCR).

28. A method of identifying viable virulent strains of *L. monocytogenes* comprising:

providing at least one primer specific for a corresponding at least one virulence-specific gene of *L. monocytogenes*;

using said at least one primer to identify said at least one gene and amplifying sequence of said gene from from mRNA by reverse transcription-PCR (RT-PCR).

29. The method of Claim 28, wherein said virulence-specific gene is selected from the group consisting of SEQ ID NOS.: 1-9.

30. A method of treating a host subject in need of treatment for the pathogenic effects of a virulent strain of *L. monocytogenes* comprising:

administering an effective amount of at least one pharmaceutically active agent that is effective in altering or inactivating the function of at least one protein encoded by a virulence-specific gene.

31. The method of Claim 30, wherein said virulence-specific gene is selected from the group consisting of SEQ ID NOS.: 1-9.

32. The method of Claim 30, wherein said altering or inactivating kills said said virulent strain of *L. monocytogenes*.

33. The method of Claim 30, wherein said altering or inactivating renders said virulent strain of *L. monocytogenes* susceptible to the immune system of said host subject.

34. A vaccine to protect a subject from the pathogenic effects of a virulent strain of *L. monocytogenes* comprising:

altering said at least one virulence-specific gene so as to render expression of the encoded protein of said at least one gene ineffective,

wherein said resulting *L. monocytogenes* is rendered avirulent and effective as a live attenuated bacteria suitable for use in a vaccine for said virulent strain of *L. monocytogenes*.

35. The method of Claim 34, wherein said virulence-specific gene is selected from the group consisting of SEQ ID NOS.: 1-9.

36. A method of vaccinating a subject to protect the subject from the pathogenic effects of a virulent strain of *L. monocytogenes* comprising:

administering a purified protein encoded by a virulence-specific gene or administering a live viral or bacterial vaccine expressing a protein encoded by a virulence-specific gene or administering a DNA vaccine comprising a virulence-specific gene.

37. The method of Claim 36, wherein said virulence-specific gene is selected from the group consisting of SEQ ID NOS.: 1-9.

38. A method of quickly determining if a sample taken from a food product contains a virulent strain of *L. monocytogenes*, the method comprising:

isolating *L. monocytogenes* from said food sample;

providing at least one primer specific for a corresponding at least one virulence-specific gene of *L. monocytogenes*;

conducting PCR assay using said at least one primer to identify the presence of said corresponding at least one virulence-specific gene in said *L. monocytogenes* isolate.

39. The method of Claim 38, wherein said virulence-specific gene is selected from the group consisting of SEQ ID NOS.: 1-9.